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Figure 1

Cloning of the endothelial cell tropic and leukotropic clinical isolate VR1814 as FIX-BAC

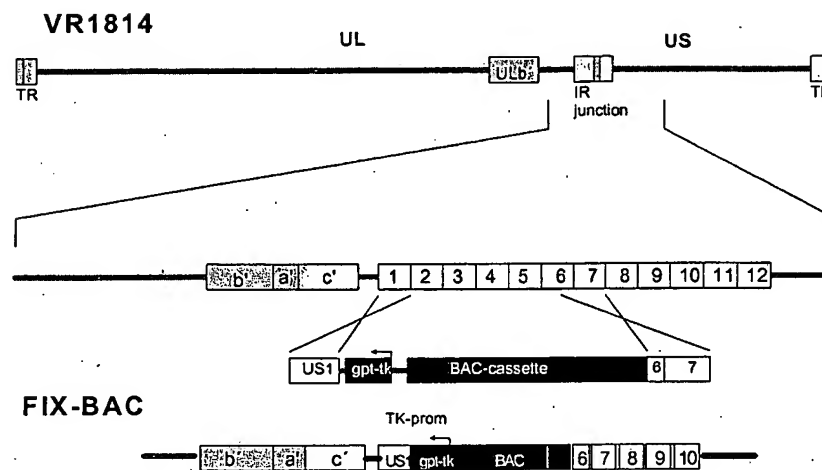


Fig. 1 Construction of FIX-BAC. A gpt-tk-BAC cassette was introduced into the US2-6 region of the parental virus VR1814 as described in patent application PCT/EP02/01867 (WO 02/066629).

Figure 2

RVFIX virus mutants	Deletion according to (Chee, Bankier et al., 1990)
RVFIX Δ ULb'	nt 175662-189347
RVFIX Δ UL132-128	nt 174857-176865
RVFIX Δ UL133-148	nt 177896-189347
RVFIX Δ UL132-130	nt 175662-177743
RVFIX Δ UL131K	nt 176377-176776
RVFIX Δ UL130	nt 175662-176314
RVFIX Δ UL128K	nt 174953-175387
RVFIX Δ UL132K	nt 177076-177752
RVFIX Δ UL148	nt 177896-178644
RVFIX Δ UL146-147	nt 179069-179966
RVFIX Δ UL127	nt 174467-174770

Fig. 2 List of RVFIX virus mutants and determination of the mutation (kanamycin cassette insertion) according to annotation by {Chee, Bankier, et al. 1990 269 /id}

Figure 3 shows an agarose gel and Southern Blot of RVFIX and RVFIX mutant viruses.

Figure 3

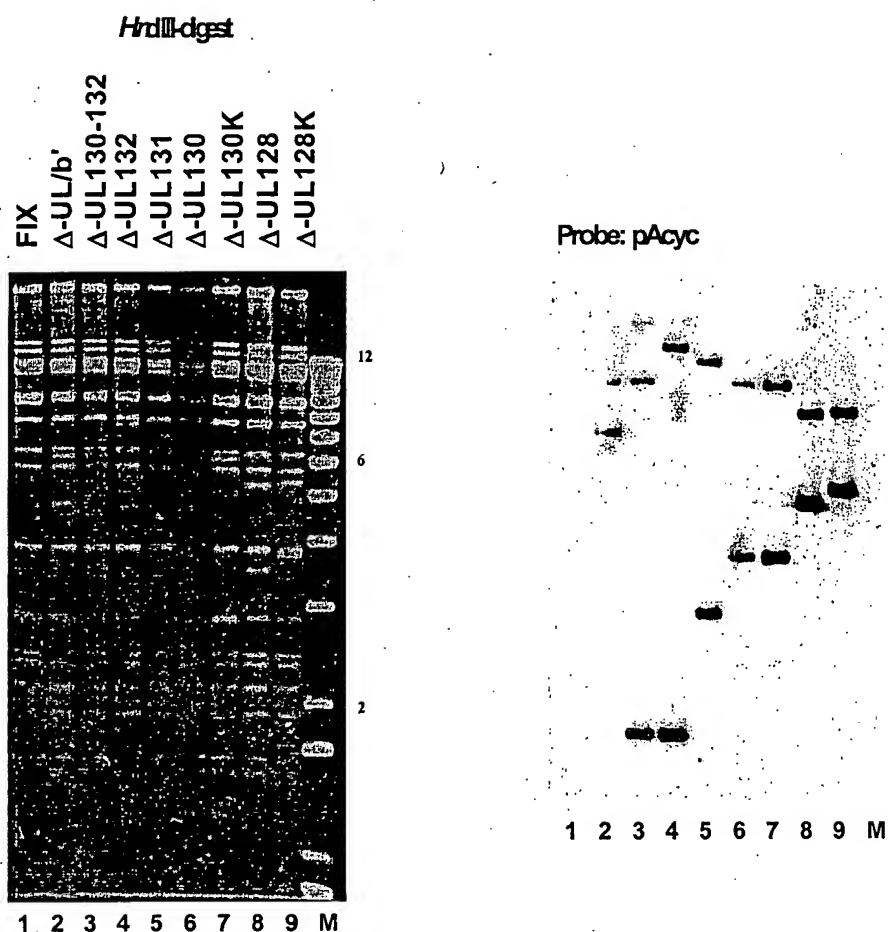


Fig.3 DNA derived from individually grown FIX-BAC clones (lane 1) or FIX-BAC mutant clones ΔULb', ΔUL130-132, ΔUL132, ΔUL131, ΔUL130, ΔUL130K, ΔUL128 and ΔUL128K (lanes 2-9) was digested with *Hind*III and run on a 0.5% agarose gel.

Figure 4

A

FIX 176834-GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGCTG
 RACE_95_3 GTCTGCAACATGCGGCTGTCTGCGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGCTG
 RACE_95_8 GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGCTG
 RACE_95_11 GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGCTG

FIX GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_3 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_8 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_11 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT

FIX GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
 RACE_95_3 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
 RACE_95_8 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
 RACE_95_11 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG

FIX TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC
 RACE_95_3 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC
 RACE_95_8 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC
 RACE_95_11 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC

FIX TCAAGAGGTTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
 RACE_95_3 TCAAGAG-----
 RACE_95_8 TCAAGAGGTTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
 RACE_95_11 TCAAGAG-----

FIX AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAATCA
 RACE_95_3 -----AATCA
 RACE_95_8 AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAATCA
 RACE_95_11 -----AATCA

FIX ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCGGCA
 RACE_95_3 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGGCGGCA
 RACE_95_8 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCGGCA
 RACE_95_11 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCGGCA

FIX CCAACAAAAGGACCACGTTCAACGCCGCCGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG
 RACE_95_3 CCAACAAAAGGACCACGTTCAACGCCGCCGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG
 RACE_95_8 CCAACAAAAGGACCACGTTCAACGCCGCCGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG
 RACE_95_11 CCAACAAAAGGACCACGTTCAACGCCGCCGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG

FIX AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA-176346
 RACE_95_3 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA
 RACE_95_8 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA
 RACE_95_11 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA

B

FIX 175631-CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_3 CCGTGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_8 CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_13 CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG

FIX7 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
 RACE_95_3 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
 RACE_95_8 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
 RACE_95_11 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC

FIX CACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA
 RACE_95_3 CACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA
 RACE_95_8 CACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA
 RACE_95_11 CACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGC-----

FIX TTTTATGATTGTCTGCGTCTGTGGTGCGTCTGGATTGTCTCTCGACGTTTCTGATAG
 RACE_95_3 TTTTCATGATTGTCTGCGTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAG
 RACE_95_8 TTTTCATGATTGTCTGCGTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAG
 RACE_95_11 -----

FIX CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
 RACE_95_3 CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
 RACE_95_8 CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
 RACE_95_11 -----GCTG

FIX CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATC
 RACE_95_3 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATC
 RACE_95_8 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATC
 RACE_95_11 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATC

FIX GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC
 RACE_95_3 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAACTGC
 RACE_95_8 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC
 RACE_95_11 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC

FIX AACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGA
 RACE_95_3 AACTACAATCC-----
 RACE_95_8 AACTACAATCC-----
 RACE_95_11 AACTACAATCT-----

FIX GGGACAAAACATCATTAATAAAAAAGTCTAATTTACAGTTTTGTACCCCCCTTCCCCTC
 RACE_95_3 -----
 RACE_95_8 -----
 RACE_95_11 -----

FIX CGTGTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
 RACE_95_3 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
 RACE_95_8 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
 RACE_95_11 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA

FIX AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT
 RACE_95_3 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT
 RACE_95_8 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT
 RACE_95_11 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT

FIX ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
 RACE_95_3 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
 RACE_95_8 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
 RACE_95_11 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAATACA

FIX AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA-174887
 RACE_95_3 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----
 RACE_95_8 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----
 RACE_95_11 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----

C

FIX 174892-CGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCGA-174841

```

RACE_95_3  -- CGCTAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCGCAAAAAAA --
RACE_95_8  -- CGCTAAATGGGCTATATGCTGCAGT AATAATAAAATGTGTGTTGTCCAAAAAA --
RACE_95_11 -- CGCTAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCAAAAAA --

```

Fig. 4 UL131-128 mRNA processing – Panels (A-C) compare FIX-BAC DNA sequence (numbered according to Chee et al.) to a set of cDNA sequences from RACE clones 95-3, 95-8 and 95-11 (A) UL131 region, (B) UL128 region, (C) UL131-128 transcripts 3' end. Start codons, stop codons and the polyA site are in bold face, mRNA processing signals (splice donor sequence, splice acceptor sequence, AATAAA signal) are grey-shaded.

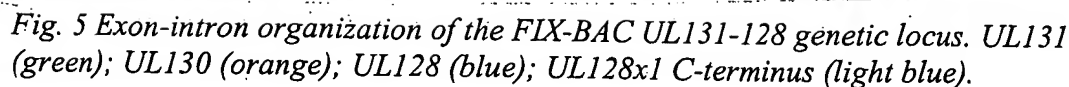


Figure 6

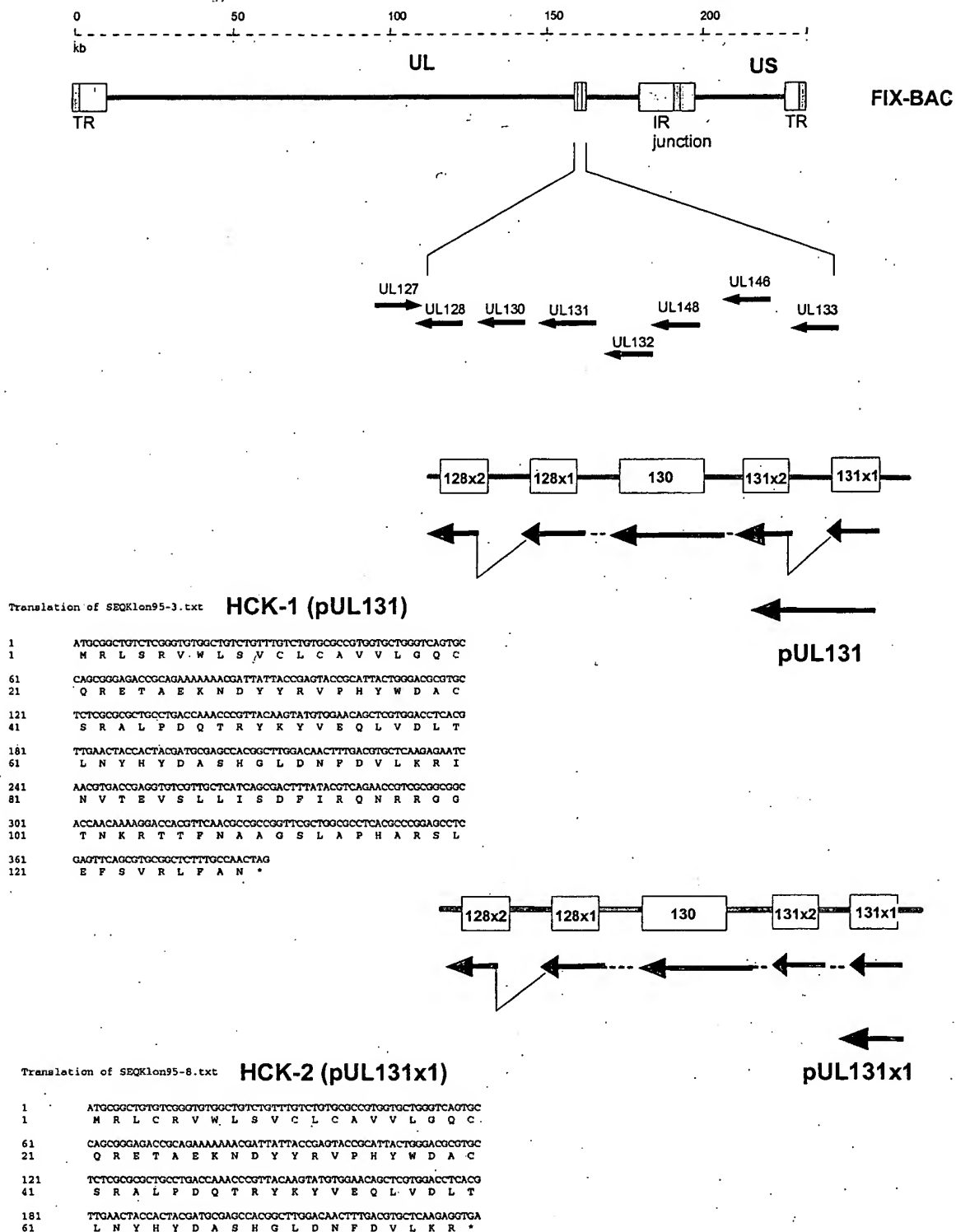
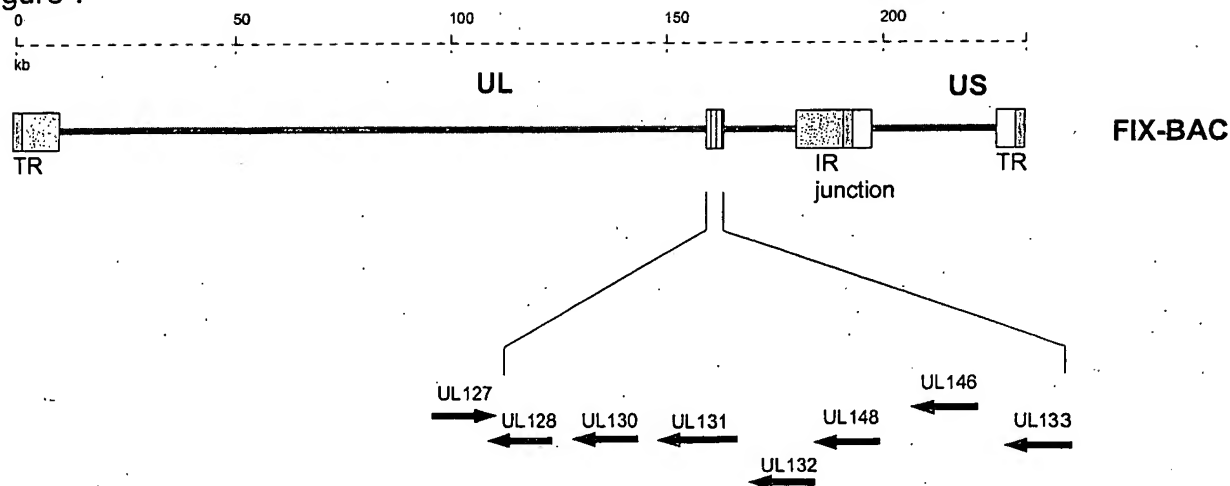


Figure 7

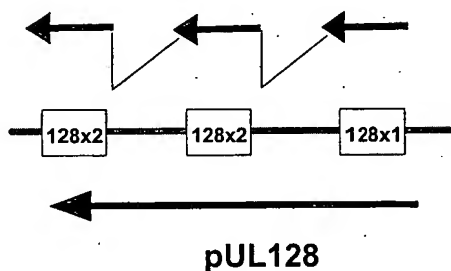


Translation of SEQ128.txt(1-563 : HCK-4 (pUL128)

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATHEGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTTACGATTTGAAAATGTGCAATCGCTTCACCGTCGCACGTGCGGTGTCCGGAC
41     E R C Y D F K M C N R P T V A L R C P D
181    GCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTTCGCGGGATCGTCACCACCATG
61     G E V C Y S P E K T A E I R G I V T T M
241    ACCCATTCATTGACACGCCAGGTGCTACACAACAACTGACGAGCTGCAACTACAATCTG
81     T H S L T R Q V V H N K L T S C N Y N L
301    TTATACCTCGAAGCTGACGGGCGAATACGCTCGGCAAAAGTGAACGACAAGGCGCAGTAC
101    L Y L E A D G R I R C G K V N D K A Q Y
361    CTGCTGGGCGCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
121    L L G A A G S V P Y R W I N L E Y D K I
421    ACCCGGATCGTGGGCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
141    T R I V G L D Q Y L E S V K K H K R L D
481    GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA
161    V C R A K M G Y M L Q *

```



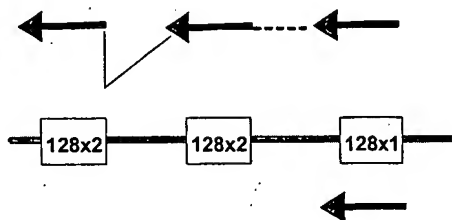
pUL128

Translation of SEQ128 x 1.txt HCK-3 (pUL128x1)

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41     E R C Y D F K M C N R P T V A Y V F S *

```



pUL128x1

Fig. 7 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel SEQUL128B and predicted open reading frame (orf) pUL128 (HCK-4). Lower panel SEQUL128A and predicted orf UL128x1 (HCK-3).

Figure 8

Northern Blot Analyses

RVFIX, RVFIX mutants and laboratory strains:

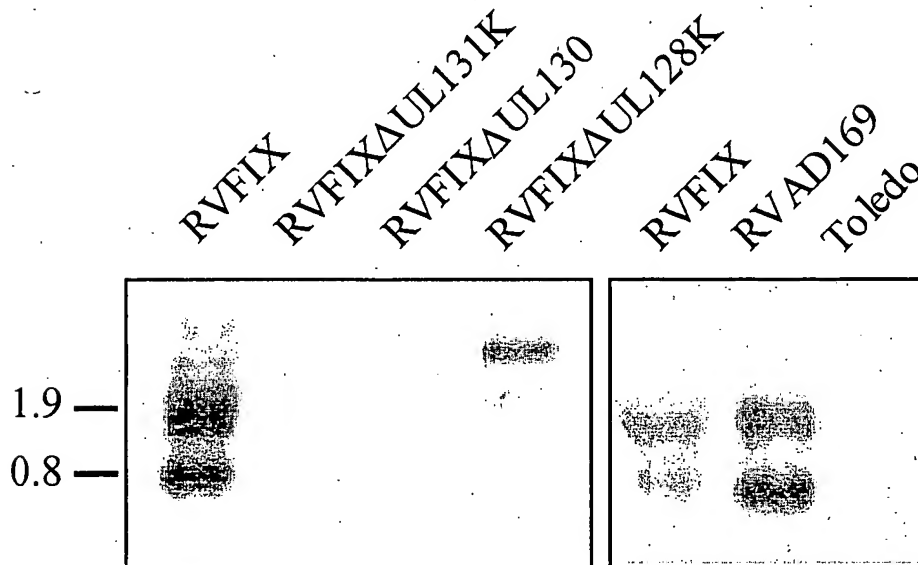


Fig. 8 mRNA was prepared from RVFIX-infected fibroblasts 4 days p.i. using Rneasy Mini, QIAshredder and Oligotex mRNA Mini kits according to the manufacturer's guidance (Qiagen). For Northern blotting, 1 μ g RNA was electrophoresed on an agarose gel according to the MOPS-formaldehyde protocol and blotted onto Hybond N+ membranes (Amersham Pharmacia). Blots were hybridized with a UL131-128 specific probe.

Figure 9

Comparison RACE clone 95-3 – FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977

Lower line: SEQKlon95-3.txt, from 1 to 1741

SEQFIX UL131-128.txt:SEQKlon95-3.txt identity= 99.66%(1735/1741)
 gap=11.94%(236/1977)

```

1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
      |||
1      .....ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG
      |||
52     GGTCAAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG

121    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
      |||
112    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC
      |||
172    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC

241    AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
      |||
232    AAGAG.....

301    CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCAAC
      |||
235    .....AATCAAC

361    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
      |||
244    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGCGGCACC

421    AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG
      |||
304    AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG

481    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
      |||
364    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
      |||
424    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

601    CGTCTCCGTGGTTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA
      |||

```

484 CGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA
 661 CGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTCTCTATCCCTCGCCCC
 |||||
 544 CGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTCTCTATCCCTCGCCCC
 721 CACGGTCCCCCTCGCAATTCCCGGGGTCCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA
 |||||
 604 CACGGTCCCCCTCGCAATTCCCGGGGTCCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA
 781 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
 |||||
 664 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
 841 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA
 |||||
 724 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGCCA
 |||||
 784 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGCCA
 961 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCACCG
 |||||
 844 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCACCG
 1021 ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG
 |||||
 904 ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG
 1081 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA
 |||||
 964 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA
 1141 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
 |||||
 1024 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
 1201 AACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
 |||||
 1084 AACCGTGCCTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
 1261 TGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
 |||||
 1144 TGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
 1321 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
 |||||
 1204 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
 1381 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGAT
 |||||
 1264 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT
 1441 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC
 |||||
 1324 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

```

1501 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA
|||||
1384 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA
|||||
1561 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCT
|||||
1444 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAACT
|||||
1621 GCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAAGTAAGACA
|||||
1504 GCAACTACAATCC.....
1681 GAGGGACAAAACATCATTAAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCC
1517 .....
1741 TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
|||||
1517 .....GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
|||||
1801 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA
|||||
1565 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA
|||||
1861 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
|||||
1625 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
|||||
1921 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
|||||
1685 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

```

Translation of SEQKlon95-3.txt: HCK-1 (pUL131)

```

1      ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTGGGTCAAGTGC
1      M R L S R V W L S V C L C A V V L G Q C
61     CAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21     Q R E T A E K N D Y Y R V P H Y W D A C
121    TCTCGCGCGCTGCCTGACCAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG
41     S R A L P D Q T R Y K Y V E Q L V D L T
181    TTGAACTACCACTACGATGCGAGCCACGGCTTGGAACAACCTTTGACGTGCTCAAGAGAATC
61     L N Y H Y D A S H G L D N F D V L K R I
241    AACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTTATACGTCAGAACCGTCGCGGCGGC
81     N V T E V S L L I S D F I R Q N R R G G
301    ACCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTC
101    T N K R T T F N A A G S L A P H A R S L
361    GAGTTCAGCGTGCGGCTCTTTGCCAACTAG
121    E F S V R L F A N *

```

Figure 10**Comparison RACE clone 95-8 –FIX genomic sequence****Upper line: SEQFIX UL131-128.txt, from 10 to 1977****Lower line: SEQKlon95-8.txt, from 1 to 1849**

SEQFIX UL131-128.txt:SEQKlon95-8.txt identity= 99.78%(1845/1849)
 gap=6.47%(128/1977)

```

1   GTCTGCAACATGCGGCTGTGTGCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1   .....ATGCGGCTGTGTGCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61  GGTCAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52  GGTCAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG

121 GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112 GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181 GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172 GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC

241 AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
232 AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA

301 CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCGAGAATCAAC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
292 CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCGAGAATCAAC

361 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
352 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC

421 AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
412 AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG

481 TTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
472 TTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541 TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
532 TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

```

601 CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA
 |||||
 592 CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA
 |||||
 661 CGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTTCTCTATCCCTCGCCCC
 |||||
 652 CGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTTCTCTATCCCTCGCCCC
 |||||
 721 CACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA
 |||||
 712 CACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA
 |||||
 781 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
 |||||
 772 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
 |||||
 841 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCGCAATCAGACCATCCTCCAACGGA
 |||||
 832 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCGCAATCAGACCATCCTCCAACGGA
 |||||
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAACGTGCAGATCAGCGTGAAGACGCCA
 |||||
 892 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAACGTGCAGATCAGCGTGAAGACGCCA
 |||||
 961 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTC AACG
 |||||
 952 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTC AACG
 |||||
 1021 ATGGCACACGTTATCAGATGTGTGTGATGAACTGGAGAGCTGGGCCCACGTCTTCCGGG
 |||||
 1012 ATGGCACACGTTATCAGATGTGTGTGATGAACTGGAGAGCTGGGCCCACGTCTTCCGGG
 |||||
 1081 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA
 |||||
 1072 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCGATAACCAGACTTACA
 |||||
 1141 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
 |||||
 1132 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
 |||||
 1201 AACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
 |||||
 1192 AACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
 |||||
 1261 TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
 |||||
 1252 TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
 |||||
 1321 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
 |||||
 1312 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
 |||||
 1381 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTGTCTCTCGACGTTTCTGAT
 |||||
 1372 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT
 |||||


```

1441 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1432 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

1501 TCGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1492 TCGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA

1561 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTTCGTACACAACAACTGACGAGCT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1552 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTTCGTACACAACAACTGACGAGCT

1621 GCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACA
      ||||||||||||
1612 GCAACTACAATCC.....

1681 GAGGGACAAAACATCATTAATAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCC
1625 .....

1741 TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1625 .....GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA

1801 CAAGGCGCAGTACCTGCTGGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1673 CAAGGCGCAGTACCTGCTGGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTGGA

1861 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
      ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
1733 ATACGACAAGATAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA

1921 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1793 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

```

Translation of SEQKlon95-8.txt: HCK-2 (pUL131x1)

```

1      ATGCGGCTGTGTGCGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGCTGGGTCAGTGC
1      M R L C R V W L S V C L C A V V L G Q C

61     CAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21     Q R E T A E K N D Y Y R V P H Y W D A C

121    TCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCAGG
41     S R A L P D Q T R Y K Y V E Q L V D L T

181    TTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTCAAGAGGTGA
61     L N Y H Y D A S H G L D N F D V L K R *

```

Figure 11**Comparison RACE clone 95-11 –FIX genomic sequence****Upper line: SEQFIX UL131-128.txt, from 10 to 1977****Lower line: SEQKlon95-11.txt, from 1 to 1620**

SEQFIX UL131-128.txt:SEQKlon95-11.txt identity= 99.57%(1611/1618)
 gap=18.24%(361/1979)

```

1      GTCTGCAACATGCGGCTGTGTCTGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      .....ATGCGGCTGTGTCTGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAAGTGCCAGCGGGAGACCGCAG...AAAAAACGATTATTACCGAGTACCGCATTACT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52     GGTCAAGTGCCAGCGGGAGACCGCAGAAAAAAAACGATTATTACCGAGTACCGCATTACT

119    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG

179    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC

239    TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
      |||||||
232    TCAAGAG.....

299    AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCA
      |||||
237    .....AATCA

359    ACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
244    ACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA

419    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
304    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG

479    AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
364    AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT

539    TCTGCTTCGTACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT

```

424 |||||TCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT
 599 GCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT
 484 |||||GCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT
 659 GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC
 544 |||||GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC
 719 CCCACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTCTG
 604 |||||CCCACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATTAACGGGTCCCGAGTGTCTG
 779 CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC
 664 |||||CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC
 839 CACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCGAATCAGACCATCCTCCAACG
 724 |||||CACCTGGGTGAAAAAGGTGATCTGGCATCTGAGCGGTGCGAATCAGACCATCCTCCAACG
 899 GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGC
 784 |||||GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGC
 959 CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCTGCAA
 844 |||||CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCTGCAA
 1019 CGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG
 904 |||||CGATGGCACACGTTATTAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG
 1079 GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTA
 964 |||||GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTA
 1139 CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTG
 1024 |||||CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTG
 1199 AAAACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT
 1084 |||||AAAACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT
 1259 ATTGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT
 1144 |||||ATTGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT
 1319 CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTA
 1204 |||||CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC..
 1379 CGTATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTG

1262
 1439 ATAGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAG
 1262
 1499 GCTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1262 ACTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGG
 1559 GATCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1321 GATCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAG
 1619 CTGCAACTACAATCCGTAAGTCTCTTCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGA
 ||||||||||||||
 1381 CTGCAACTACAATCT.....
 1679 CAGAGGGACAAAACATCATTAATAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCC
 1396
 1739 CCTCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1396GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC
 1799 GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1442 GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG
 1859 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1502 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA
 1919 CACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1562 TACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

*Figure 12***Comparison SEQ 128 B - FIX genomic sequence**

Upper line: FIX genomic sequence

Lower line: SEQ 128 B

```

5998  ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058  CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118  GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA

6178  TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181    TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC

6238  ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241    ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG

6298  GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301    GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC

6358  ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361    ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT

6418  CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
      ||
421    CC.....

6478  CATCATTAATAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCCTCCGTGTTGTA
      ||
423    .....

```

```

6538  GGT TATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
      |||
423   . GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598  ACCTGCTGGGCGCCGCTGGCGGCGTTCCTATCGATGGATCAACCTGGAATACGACAAGA
      |||
482   ACCTGCTGGGCGCCGCTGGCGGCGTTCCTATCGATGGATCAACCTGGAATACGACAAGA

6658  TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
      |||
542   TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG

6718  ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC
      |||
602   ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC

6778  GAAATACGCGTTTTTGAGATTTCTG
      |||
662   AAAAAAAAAAAAAAAAAAAAAA

```

Translation of SEQ128 B x 1.txt: HCK-3 (pUL128x1)

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S

61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P

121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41     E R C Y D F K M C N R F T V A Y V F S *

```

Figure 13

Comparison SEQ 128 A - FIX genomic sequence**Upper line: FIX-BAC****Lower line: SEQ128 A**

```

5998  ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058  CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118  GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTATGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC.....

6178  TTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGATAGCCATGTTCC

166    .....

6238  ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
      |||||||||||||||
166    .....GCTGCGGTGTCCG

6298  GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATCGTCACCACC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
178    GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGATCGTCACCACC

6358  ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
238    ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT

6418  CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
      ||
298    CC.....

6478  CATCATTAATAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCCTCCGTGTTGTA

300    .....

6538  GGTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
300    .GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598  ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

359 ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
 6658 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 419 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
 6718 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 479 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTG

Translation of SEQ128 A: HCK-4 (pUL128)

1 ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTACAGC
 1 M S P K N L T P F L T A L W L L L G H S
 61 CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
 21 R V P R V R A E E C C E F I N V N H P P
 121 GAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCACTGCGGTGTCCGGAC
 41 E R C Y D F K M C N R F T V A L R C P D
 181 GGCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTCGCGGGATCGTCACCACCATG
 61 G E V C Y S P E K T A E I R G I V T T M
 241 ACCCATTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAATCTG
 81 T H S L T R Q V V H N K L T S C N Y N L
 301 TTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGTAC
 101 L Y L E A D G R I R C G K V N D K A Q Y
 361 CTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
 121 L L G A A G S V P Y R W I N L E Y D K I
 421 ACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
 141 T R I V G L D Q Y L E S V K K H K R L D
 481 GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA
 161 V C R A K M G Y M L Q *

Figure 14

Translation of SEQUL130: HCK-5 (pUL130)

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1      ATGCTACGGCTTCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCA
1      M L R L L L R H H F H C L L L C A V W A

61     ACGCCCTGTCTGGCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCA
21     T P C L A S P W F T L T A N Q N P S P P

121    TGGTCTAAACTGACGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTTCTC
41     W S K L T Y P K P H D A A T F Y C P F L

181    TATCCCTCGCCCCACGGTCCCCCTCGCAATTCCCGGGTTCCAGCGGGTATCAACGGGT
61     Y P S P P R S P S Q F P G F Q R V S T G

241    CCCGAGTGTGCAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTG
81     P E C R N E T L Y L L Y N R E G Q T L V

301    GAGAGAAGCTCCACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACC
101    E R S S T W V K K V I W Y L S G R N Q T

361    ATCCTCCAACGGATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGC
121    I L Q R M P R T A S K P S D G N V Q I S

421    GTGGAAGACGCCAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGT
141    V E D A K I F G A H M V P K Q T K L L R

481    TTCGTCGTCAACGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCC
161    F V V N D G T R Y Q M C V M K L E S W A

541    CACGTCTTCCGGGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAAT
181    H V F R D Y S V S F Q V R L T F T E A N

601    AACCAGACTTACACCTTCTGCACCCATCCCAATCTCATCGTTTGA
201    N Q T Y T F C T H P N L I V *

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